



IFWO

RAW SEQUENCE LISTING

DATE: 07/22/2004

PATENT APPLICATION: US/10/689,677C

TIME: 09:43:46

Input Set : A:\08702.0093.ST25.txt

Output Set : N:\CRF4\07222004\J689677C.raw

3 <110> APPLICANT: Wolfman, Neil
 4 Bouxsein, Mary
 6 <120> TITLE OF INVENTION: ActRIIB Fusion Polypeptides and Uses Therefor
 8 <130> FILE REFERENCE: 08702.0093-00000
 10 <140> CURRENT APPLICATION NUMBER: US 10/689,677C
 11 <141> CURRENT FILING DATE: 2003-10-22
 13 <150> PRIOR APPLICATION NUMBER: US 60/421,041
 14 <151> PRIOR FILING DATE: 2002-10-25
 16 <160> NUMBER OF SEQ ID NOS: 6
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 512
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Human
 25 <400> SEQUENCE: 1
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 31 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
 32 20 25 30
 35 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
 36 35 40 45
 39 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Ala
 40 50 55 60
 43 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
 44 65 70 75 80
 47 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
 48 85 90 95
 51 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
 52 100 105 110
 55 Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val Thr Tyr Glu Pro
 56 115 120 125
 59 Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
 60 130 135 140
 63 Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
 64 145 150 155 160
 67 Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Asp Pro
 68 165 170 175
 71 Gly Pro Pro Pro Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu
 72 180 185 190
 75 Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Gln
 76 195 200 205
 79 Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp Lys
 80 210 215 220



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83 Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met Lys
84 225                230                235                240
87 His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn
88                245                250                255
91 Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser
92                260                265                270
95 Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu Cys
96                275                280                285
99 His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu Asp
100                290                295                300
103 Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His Arg
104 305                310                315                320
107 Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala Val
108                325                330                335
111 Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro
112                340                345                350
115 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu
116                355                360                365
119 Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg Ile
120                370                375                380
123 Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Val Ser Arg Cys
124 385                390                395                400
127 Lys Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu Glu
128                405                410                415
131 Glu Ile Gly Gln His Pro Ser Leu Glu Glu Leu Gln Glu Val Val Val
132                420                425                430
135 His Lys Lys Met Arg Pro Thr Ile Lys Asp His Trp Leu Lys His Pro
136                435                440                445
139 Gly Leu Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp
140                450                455                460
143 Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Val Ser Leu
144 465                470                475                480
147 Ile Arg Arg Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Leu
148                485                490                495
151 Val Thr Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile
152                500                505                510
155 <210> SEQ ID NO: 2
156 <211> LENGTH: 375
157 <212> TYPE: PRT
158 <213> ORGANISM: Human
160 <400> SEQUENCE: 2
162 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
163 1                5                10                15
166 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
167                20                25                30
170 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
171                35                40                45
174 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
175                50                55                60

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178 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
179 65          70          75          80
182 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
183          85          90          95
186 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
187          100         105         110
190 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
191          115         120         125
194 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
195          130         135         140
198 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
199 145          150         155         160
202 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
203          165         170         175
206 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
207          180         185         190
210 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
211          195         200         205
214 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
215          210         215         220
218 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
219 225          230         235         240
222 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
223          245         250         255
226 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
227          260         265         270
230 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
231          275         280         285
234 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
235          290         295         300
238 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
239 305          310         315         320
242 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
243          325         330         335
246 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
247          340         345         350
250 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
251          355         360         365
254 Val Asp Arg Cys Gly Cys Ser
255          370         375
258 <210> SEQ ID NO: 3
259 <211> LENGTH: 378
260 <212> TYPE: PRT
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Chimera/Fusion
266 <400> SEQUENCE: 3
268 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
269 1          5          10          15

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272 Ser Tyr Ile Tyr Ala Thr Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu
273      20      25      30
276 Cys Ile Tyr Tyr Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser
277      35      40      45
280 Gly Leu Glu Arg Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr
281      50      55      60
284 Ala Ser Trp Arg Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly
285 65      70      75      80
288 Cys Trp Leu Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala
289      85      90      95
292 Thr Glu Glu Asn Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe
293     100     105     110
296 Cys Asn Glu Arg Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val
297     115     120     125
300 Thr Tyr Glu Pro Pro Pro Thr Ala Pro Thr Gly Gly Arg Gly Asp Asp
301     130     135     140
304 Asp Asp Lys Thr Arg Ser Arg Asp Lys Thr His Thr Cys Pro Pro Cys
305 145     150     155     160
308 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
309     165     170     175
312 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
313     180     185     190
316 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
317     195     200     205
320 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
321     210     215     220
324 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 225     230     235     240
328 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
329     245     250     255
332 Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
333     260     265     270
336 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
337     275     280     285
340 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
341     290     295     300
344 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
345 305     310     315     320
348 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
349     325     330     335
352 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
353     340     345     350
356 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
357     355     360     365
360 Gln Lys Ser Leu Ser Leu Ser Pro Pro Lys
361     370     375
364 <210> SEQ ID NO: 4
365 <211> LENGTH: 1134
366 <212> TYPE: DNA

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367 <213> ORGANISM: Artificial Sequence

369 <220> FEATURE:

370 <223> OTHER INFORMATION: Chimera/Fusion

372 <400> SEQUENCE: 4

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373 atgaaattct tagtcaacgt tgcccttggt tttatggctg tgtacatttc ttacatctat      60
375 gcgactagtg ggcgtgggga ggctgagaca cgggagtgca tctactacaa cgccaactgg      120
377 gagctggagc gcaccaacca gagcggcctg gagcgctgcg aaggcgagca ggacaagcgg      180
379 ctgcactgct acgcctcctg gcgcaacagc tctggcacca tcgagctcgt gaagaagggc      240
381 tgctggctag atgacttcaa ctgctacgat aggcaggagt gtgtggccac tgaggagaac      300
383 cccaggtgt acttctgctg ctgtgaaggc aacttctgca acgagcgctt cactcatttg      360
385 ccagaggctg gggggccgga agtcacgtac gagccacccc cgacagcccc caccggcggc      420
387 cgcggagacg acgacgacaa gacgcgttct agagacaaaa ctcacacatg cccaccgtgc      480
389 ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaaa acccaaggac      540
391 accctcatga tctcccggac ccctgaggtc acatgcgtgg tggaggacgt gagccacgaa      600
393 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca      660
395 aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgctct caccgtcctg      720
397 caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca      780
399 gtccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac      840
401 accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc      900
403 aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaa      960
405 aactacaaga ccacgcctcc cgtgctggac tccgacgget ccttcttctt ctatagcaag      1020
407 ctacaccgtg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat      1080
409 gaggtctgct acaaccacta cagcagaag agcctctccc tgtccccgcc taaa          1134

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412 <210> SEQ ID NO: 5

413 <211> LENGTH: 4

414 <212> TYPE: PRT

415 <213> ORGANISM: Artificial Sequence

417 <220> FEATURE:

418 <223> OTHER INFORMATION: Linking Sequence, Gly-Ser repeat

420 <400> SEQUENCE: 5

422 Gly Ser Gly Ser

423 1

426 <210> SEQ ID NO: 6

427 <211> LENGTH: 4

428 <212> TYPE: PRT

429 <213> ORGANISM: Artificial Sequence

431 <220> FEATURE:

432 <223> OTHER INFORMATION: Linking Sequence, Enterokinase Cleavage Site

434 <400> SEQUENCE: 6

436 Asp Asp Asp Lys

437 1

VERIFICATION SUMMARY

DATE: 07/22/2004

PATENT APPLICATION: US/10/689,677C

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Input Set : A:\08702.0093.ST25.txt

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